

WHAT IS CLAIMED IS:

1. An isolated protein complex having a first protein which is FHOS or a homologue or derivative or fragment thereof interacting with a second protein  
5 selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip,  
10 TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b,  
15 m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof.

2. The isolated protein complex of Claim 1, wherein said first protein is FHOS.

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3. The isolated protein complex of Claim 1, wherein said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK.

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4. The isolated protein complex of Claim 1, wherein said first protein is FHOS, and said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK.
5. The isolated protein complex of Claim 1, wherein said first protein comprises an amino acid sequence selected from the group consisting of:
- a first sequence consisting of the amino acids as set forth in Figure 1;
  - a second sequence consisting of the amino acids as set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117;
  - a third sequence consisting of the amino acids identical to that set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 the third sequence has one or more conservative amino acid substitutions;
  - a fourth sequence consisting of the amino acids identical to that set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117, the fourth sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not alter its interacting property with the second protein;
  - a fifth sequence consisting of the amino acids identical to that set forth in Figure 1 except that, over the entire length corresponding to the amino acid sequence of Figure 1, the fifth sequence has one or more conservative amino acid

substitutions; and

- (f) a sixth sequence consisting of the amino acids identical to that set forth in Figure 1 except that, over the entire length corresponding to the amino acid sequence of Figure 1, the sixth sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not alter its interacting property with the second protein.

6. The isolated protein complex of Claim 1, wherein said second protein comprises an amino acid sequence selected from the group consisting of:

- (a) a first sequence consisting of the amino acids as set forth in any of Figures 2-23, 27-53, and 58-77; (b) a second sequence consisting of the amino acids as set forth in any of SEQ ID NOS: 4-26, 55-86, and 118-138;
- (c) a third sequence consisting of the amino acids identical to that set forth in any of SEQ ID NOS: 4-26, 55-86, and 118-138; except that, over the entire length corresponding to the amino acid sequence of SEQ ID NOS: 4-26, 55-86, and 118-138; the third sequence has one or more conservative amino acid substitutions;
- (d) a fourth sequence consisting of the amino acids identical to that set forth in any of SEQ ID NOS: 4-26, 55-86, and 118-138; except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 4-26, 55-86, and 118-138; the fourth sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not render it unable to interact with the first protein;
- (e) a fifth sequence consisting of the amino acids identical to that set forth in any of Figures 2-23, 27-53, and 58-77; except that, over the entire length corresponding to the amino acid sequence of Figures 2-23, 27-53, and 58-77 the fifth sequence has one or more conservative amino acid substitutions; and
- (f) a sixth sequence consisting of the amino acids identical to that set forth in any of Figures 2-23, 27-53, and 58-77, except that, over the entire length corresponding to the amino acid sequence of any of Figures 2-23, 27-53, and 58-77; the sixth sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not render it unable to interact with the first protein.

7. The isolated protein complex of Claim 1, wherein said first protein

is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not  
5 render it unable to interact with mRNF23,  
and wherein said second protein is mRNF23 comprising:
  - (c) an amino acid sequence set forth in Figure 2;
  - (d) a sequence having a truncation of up to 100 amino acids at the N-terminus or up to 254 amino acids at the C-terminus of the sequence set forth in  
10 Figure 2, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 100 amino acids at the N-terminus and up to 254 amino acids at the C-terminus of the sequence set forth in Figure 2, such that the truncation does not render it unable to interact with FHOS.

15           8.       The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not  
20 render it unable to interact with mERp59,  
and wherein said second protein is mERp59 comprising:
  - (c) an amino acid sequence set forth in Figure 3;
  - (d) a sequence having a truncation of up to 22 amino acids at the N-terminus or up to 184 amino acids at the C-terminus of the sequence set forth in  
25 Figure 3, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 22 amino acids at the N-terminus and up to 184 amino acids at the C-terminus of the sequence set forth in Figure 3, such that the truncation does not render it unable to interact with FHOS.

30           9.       The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not

render it unable to interact with mBRD7(621),

and wherein said second protein is mBRD7(621) comprising:

(c) an amino acid sequence set forth in Figure 4;

(d) a sequence having a truncation of up to 42 amino acids at the

5 N-terminus or up to 310 amino acids at the C-terminus of the sequence set forth in Figure 4, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 42 amino acids at the

N-terminus and up to 310 amino acids at the C-terminus of the sequence set forth in Figure 4, such that the truncation does not render it unable to interact with FHOS.

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10. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 1014 amino acids at the

15 C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mSPNA1,

and wherein said second protein is mSPNA1 comprising:

(c) an amino acid sequence set forth in Figure 5;

(d) a sequence having a truncation of up to 453 amino acids at the

20 N-terminus or up to 1738 amino acids at the C-terminus of the sequence set forth in Figure 5, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 453 amino acids at the

N-terminus and up to 1738 amino acids at the C-terminus of the sequence set forth in Figure 5, such that the truncation does not render it unable to interact with FHOS.

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11. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 1014 amino acids at the

30 C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mVCP,

and wherein said second protein is mVCP comprising:

(c) an amino acid sequence set forth in Figure 6;

(d) a sequence having a truncation of up to 477 amino acids at the

N-terminus or up to 9 amino acids at the C-terminus of the sequence set forth in Figure 6, such that the truncation does not render it unable to interact with FHOS; or

- (e) a sequence having a truncation of up to 477 amino acids at the N-terminus and up to 9 amino acids at the C-terminus of the sequence set forth in Figure 6, such that the truncation does not render it unable to interact with FHOS.

12. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mSTAT5A,  
and wherein said second protein is mSTAT5A comprising:
  - (c) an amino acid sequence set forth in Figure 7;
  - (d) a sequence having a truncation of up to 31 amino acids at the N-terminus or up to 474 amino acids at the C-terminus of the sequence set forth in Figure 7, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 31 amino acids at the N-terminus and up to 474 amino acids at the C-terminus of the sequence set forth in Figure 7, such that the truncation does not render it unable to interact with FHOS.

13. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mTAKEDA009,  
and wherein said second protein is mTAKEDA009 comprising:
  - (c) an amino acid sequence set forth in Figure 8.

14. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the

C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mPTRF,

and wherein said second protein is mPTRF comprising:

- (c) an amino acid sequence set forth in Figure 9;
- 5 (d) a sequence having a truncation of up to 24 amino acids at the N-terminus or up to 262 amino acids at the C-terminus of the sequence set forth in Figure 9, such that the truncation does not render it unable to interact with FHOS; or
- (e) a sequence having a truncation of up to 24 amino acids at the N-terminus and up to 262 amino acids at the C-terminus of the sequence set forth in
- 10 Figure 9, such that the truncation does not render it unable to interact with FHOS.

15. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
  - 15 (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mAK031693,
- and wherein said second protein is mAK031693 comprising:
- (c) an amino acid sequence set forth in Figure 10;
  - 20 (d) a sequence having a truncation of up to 71 amino acids at the N-terminus or up to 79 amino acids at the C-terminus of the sequence set forth in Figure 10, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 71 amino acids at the N-terminus and up to 79 amino acids at the C-terminus of the sequence set forth in
  - 25 Figure 10, such that the truncation does not render it unable to interact with FHOS.

16. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- 30 (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m1200014P03Rik,

and wherein said second protein is m1200014P03Rik comprising:

- (c) an amino acid sequence set forth in Figure 11;

(d) a sequence having a truncation of up to 252 amino acids at the N-terminus or up to 73 amino acids at the C-terminus of the sequence set forth in Figure 11, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 252 amino acids at the N-terminus and up to 73 amino acids at the C-terminus of the sequence set forth in Figure 11, such that the truncation does not render it unable to interact with FHOS.

17. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mNNP1,

and wherein said second protein is mNNP1 comprising:

(c) an amino acid sequence set forth in Figure 12;

(d) a sequence having a truncation of up to 40 amino acids at the N-terminus or up to 103 amino acids at the C-terminus of the sequence set forth in Figure 12, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 40 amino acids at the N-terminus and up to 103 amino acids at the C-terminus of the sequence set forth in Figure 12, such that the truncation does not render it unable to interact with FHOS.

18. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mLOC213473(195),

and wherein said second protein is mLOC213473(195) comprising:

(c) an amino acid sequence set forth in Figure 13.

19. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or



(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mGOLGA3,

and wherein said second protein is mGOLGA3 comprising:

5 (c) an amino acid sequence set forth in Figure 14;

(d) a sequence having a truncation of up to 819 amino acids at the N-terminus or up to 428 amino acids at the C-terminus of the sequence set forth in Figure 14, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 819 amino acids at the  
10 N-terminus and up to 428 amino acids at the C-terminus of the sequence set forth in Figure 14, such that the truncation does not render it unable to interact with FHOS.

20. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

15 (a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mMYG1-pending,

and wherein said second protein is mMYG1-pending comprising:

20 (c) an amino acid sequence set forth in Figure 15;

(d) a sequence having a truncation of up to 48 amino acids at the N-terminus or up to 12 amino acids at the C-terminus of the sequence set forth in Figure 15, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 48 amino acids at the  
25 N-terminus and up to 12 amino acids at the C-terminus of the sequence set forth in Figure 15, such that the truncation does not render it unable to interact with FHOS.

21. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

30 (a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mAK044679(668),

and wherein said second protein is mAK044679(668) comprising:

- (c) an amino acid sequence set forth in Figure 16; or
- (d) a sequence having a truncation of up to 425 amino acids at the C-terminus of the sequence set forth in Figure 16, such that the truncation does not render it unable to interact with FHOS.

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22. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with RS21C6,

and wherein said second protein is RS21C6 comprising:

- (c) an amino acid sequence set forth in Figure 17; or
- (d) a sequence having a truncation of up to 68 amino acids at the N-terminus of the sequence set forth in Figure 17, such that the truncation does not render it unable to interact with FHOS.

23. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with KIAA0562,

and wherein said second protein is KIAA0562 comprising:

- (c) an amino acid sequence set forth in Figure 18;
- (d) a sequence having a truncation of up to 263 amino acids at the N-terminus or up to 290 amino acids at the C-terminus of the sequence set forth in Figure 18, such that the truncation does not render it unable to interact with FHOS; or
- (e) a sequence having a truncation of up to 263 amino acids at the N-terminus and up to 290 amino acids at the C-terminus of the sequence set forth in Figure 18, such that the truncation does not render it unable to interact with FHOS.

24. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or  
(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with COPB,

5 and wherein said second protein is COPB comprising:

(c) an amino acid sequence set forth in Figure 19;  
(d) a sequence having a truncation of up to 305 amino acids at the N-terminus or up to 85 amino acids at the C-terminus of the sequence set forth in Figure 19, such that the truncation does not render it unable to interact with FHOS; or  
10 (e) a sequence having a truncation of up to 305 amino acids at the N-terminus and up to 85 amino acids at the C-terminus of the sequence set forth in Figure 19, such that the truncation does not render it unable to interact with FHOS.

25. The isolated protein complex of Claim 1, wherein said first protein  
15 is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or  
(b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MYH7,  
20 and wherein said second protein is MYH7 comprising:  
(c) an amino acid sequence set forth in Figure 20;  
(d) a sequence having a truncation of up to 1249 amino acids at the N-terminus or up to 316 amino acids at the C-terminus of the sequence set forth in Figure 20, such that the truncation does not render it unable to interact with FHOS;  
25 (e) a sequence having a truncation of up to 1249 amino acids at the N-terminus and up to 316 amino acids at the C-terminus of the sequence set forth in Figure 20, such that the truncation does not render it unable to interact with FHOS;  
(f) a sequence having a truncation of up to 819 amino acids at the N-terminus or up to 897 amino acids at the C-terminus of the sequence set forth in  
30 Figure 20, such that the truncation does not render it unable to interact with FHOS; or  
(g) a sequence having a truncation of up to 819 amino acids at the N-terminus and up to 897 amino acids at the C-terminus of the sequence set forth in Figure 20, such that the truncation does not render it unable to interact with FHOS;

26. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
  - (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with KIAA1633,
- and wherein said second protein is KIAA1633 comprising:
- (c) an amino acid sequence set forth in Figure 21;
  - (d) a sequence having a truncation of up to 242 amino acids at the N-terminus or up to 1155 amino acids at the C-terminus of the sequence set forth in Figure 21, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 242 amino acids at the N-terminus and up to 1155 amino acids at the C-terminus of the sequence set forth in Figure 21, such that the truncation does not render it unable to interact with FHOS.

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27. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
  - (b) a sequence having a truncation of up to 1014 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with KIAA1288(1191),
- and wherein said second protein is KIAA1288(1191) comprising:
- (c) an amino acid sequence set forth in Figure 22;
  - (d) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 113 amino acids at the C-terminus of the sequence set forth in Figure 22, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 651 amino acids at the N-terminus and up to 113 amino acids at the C-terminus of the sequence set forth in Figure 22, such that the truncation does not render it unable to interact with FHOS.

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28. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 914 amino acids at the

C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mVCL,

and wherein said second protein is mVCL comprising:

- (c) an amino acid sequence set forth in Figure 23;
- 5 (d) a sequence having a truncation of up to 28 amino acids at the N-terminus or up to 591 amino acids at the C-terminus of the sequence set forth in Figure 23, such that the truncation does not render it unable to interact with FHOS; or
- (e) a sequence having a truncation of up to 28 amino acids at the N-terminus and up to 591 amino acids at the C-terminus of the sequence set forth in
- 10 Figure 23, such that the truncation does not render it unable to interact with FHOS.

29. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
  - 15 (b) a sequence having a truncation of up to 816 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mBC028274(908),
- and wherein said second protein is mBC028274(908) comprising:
- (c) an amino acid sequence set forth in Figure 27;
  - 20 (d) a sequence having a truncation of up to 249 amino acids at the N-terminus or up to 343 amino acids at the C-terminus of the sequence set forth in Figure 2, such that the truncation does not render it unable to interact with FHOS; or
  - (e) a sequence having a truncation of up to 249 amino acids at the N-terminus and up to 343 amino acids at the C-terminus of the sequence set forth in
  - 25 Figure 27, such that the truncation does not render it unable to interact with FHOS.

30. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- 30 (b) a sequence having a truncation of up to 816 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mBC026864(777),

and wherein said second protein is mBC026864(777) comprising:

- (c) an amino acid sequence set forth in Figure 28;

(d) a sequence having a truncation of up to 255 amino acids at the N-terminus or up to 360 amino acids at the C-terminus of the sequence set forth in Figure 3, such that the truncation does not render it unable to interact with FHOS; or

5 (e) a sequence having a truncation of up to 255 amino acids at the N-terminus and up to 360 amino acids at the C-terminus of the sequence set forth in Figure 28, such that the truncation does not render it unable to interact with FHOS.

31. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

10 (a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 816 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m5730504C04Rik,

and wherein said second protein is m5730504C04Rik comprising:

15 (c) an amino acid sequence set forth in Figure 29;

(d) a sequence having a truncation of up to 126 amino acids at the N-terminus or up to 829 amino acids at the C-terminus of the sequence set forth in Figure 4, such that the truncation does not render it unable to interact with FHOS; or

20 (e) a sequence having a truncation of up to 126 amino acids at the N-terminus and up to 829 amino acids at the C-terminus of the sequence set forth in Figure 29, such that the truncation does not render it unable to interact with FHOS.

32. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

25 (a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 816 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mMYH9,

and wherein said second protein is mMYH9 comprising:

30 (c) an amino acid sequence set forth in Figure 30;

(d) a sequence having a truncation of up to 852 amino acids at the N-terminus or up to 769 amino acids at the C-terminus of the sequence set forth in Figure 30, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 852 amino acids at the

N-terminus and up to 769 amino acids at the C-terminus of the sequence set forth in Figure 5, such that the truncation does not render it unable to interact with FHOS.

33. The isolated protein complex of Claim 1, wherein said first protein  
5 is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 816 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mp116Rip,

10 and wherein said second protein is mp116Rip comprising:

- (c) an amino acid sequence set forth in Figure 31; or
- (d) a sequence having a truncation of up to 942 amino acids at the N-terminus of the sequence set forth in Figure 31, such that the truncation does not render it unable to interact with FHOS.

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34. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 816 amino acids at the  
20 C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with TPM3,

and wherein said second protein is TPM3 comprising:

- (c) an amino acid sequence set forth in Figure 32; or
- (d) a sequence having a truncation of up to 156 amino acids at the  
25 N-terminus of the sequence set forth in Figure 32, such that the truncation does not render it unable to interact with FHOS.

35. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 816 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MYH6,

and wherein said second protein is MYH6 comprising:

- (c) an amino acid sequence set forth in Figure 33;
- (d) a sequence having a truncation of up to 875 amino acids at the N-terminus or up to 826 amino acids at the C-terminus of the sequence set forth in Figure 8, such that the truncation does not render it unable to interact with FHOS; or
- 5 (e) a sequence having a truncation of up to 875 amino acids at the N-terminus and up to 826 amino acids at the C-terminus of the sequence set forth in Figure 33, such that the truncation does not render it unable to interact with FHOS.

36. The isolated protein complex of Claim 1, wherein said first protein  
10 is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mMBLR;
- 15 or
- (c) a sequence having a truncation of up to 651 amino acids at the N-terminus and up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mMBLR, and wherein said second protein is mMBLR comprising:
- 20 (d) an amino acid sequence set forth in Figure 34;
- (e) a sequence having a truncation of up to 40 amino acids at the N-terminus or up to 144 amino acids at the C-terminus of the sequence set forth in Figure 34, such that the truncation does not render it unable to interact with FHOS; or
- (f) a sequence having a truncation of up to 40 amino acids at the
- 25 N-terminus and up to 144 amino acids at the C-terminus of the sequence set forth in Figure 34, such that the truncation does not render it unable to interact with FHOS.

37. The isolated protein complex of Claim 1, wherein said first protein  
is FHOS comprising:

- 30 (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mZFP144;

or



- (c) a sequence having a truncation of up to 651 amino acids at the N-terminus and up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mZFP144, and wherein said second protein is mZFP144 comprising:
- 5 (d) an amino acid sequence set forth in Figure 35;
- (e) a sequence having a truncation of up to 6 amino acids at the N-terminus or up to 38 amino acids at the C-terminus of the sequence set forth in Figure 35, such that the truncation does not render it unable to interact with FHOS; or
- (f) a sequence having a truncation of up to 6 amino acids at the
- 10 N-terminus and up to 38 amino acids at the C-terminus of the sequence set forth in Figure 35, such that the truncation does not render it unable to interact with FHOS.

38. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:
- 15 (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with ZNF144(294); or
- 20 (c) a sequence having a truncation of up to 651 amino acids at the N-terminus and up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with ZNF144(294),
- and wherein said second protein is ZNF144(294) comprising:
- 25 (d) an amino acid sequence set forth in Figure 35.

39. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:
- (a) an amino acid sequence set forth in Figure 1; or
- 30 (b) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3epsilon;
- (c) a sequence having a truncation of up to 651 amino acids at the

N-terminus and up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3epsilon;

(d) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3epsilon; or

(e) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3epsilon,

and wherein said second protein is 14-3-3epsilon comprising:

(f) an amino acid sequence set forth in Figure 37;

(g) a sequence having a truncation of up to 88 amino acids at the N-terminus or up to 17 amino acids at the C-terminus of the sequence set forth in Figure 37, such that the truncation does not render it unable to interact with FHOS; or

(h) a sequence having a truncation of up to 88 amino acids at the N-terminus and up to 17 amino acids at the C-terminus of the sequence set forth in Figure 12, such that the truncation does not render it unable to interact with FHOS.

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40. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with BF672897(87); or

(c) a sequence having a truncation of up to 651 amino acids at the N-terminus and up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with BF672897(87),

and wherein said second protein is BF672897(87) comprising:

(d) an amino acid sequence set forth in Figure 38.

41. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:
- (a) an amino acid sequence set forth in Figure 1;
  - (b) a sequence having a truncation of up to 651 amino acids at the N-terminus or up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mCATNB; or
  - (c) a sequence having a truncation of up to 651 amino acids at the N-terminus and up to 354 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mCATNB, and wherein said second protein is mCATNB comprising:
    - (d) an amino acid sequence set forth in Figure 39;
    - (e) a sequence having a truncation of up to 27 amino acids at the N-terminus or up to 493 amino acids at the C-terminus of the sequence set forth in Figure 14, such that the truncation does not render it unable to interact with FHOS; or
    - (f) a sequence having a truncation of up to 27 amino acids at the N-terminus and up to 493 amino acids at the C-terminus of the sequence set forth in Figure 39, such that the truncation does not render it unable to interact with FHOS.
42. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:
- (a) an amino acid sequence set forth in Figure 1;
  - (b) a sequence having a truncation of up to 250 amino acids at the N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mCATNS; or
  - (c) a sequence having a truncation of up to 250 amino acids at the N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mCATNS, and wherein said second protein is mCATNS comprising:
    - (d) an amino acid sequence set forth in Figure 40; or
    - (e) a sequence having a truncation of up to 703 amino acids at the N-terminus or up to 40 amino acids at the C-terminus of the sequence set forth in Figure 40, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 703 amino acids at the N-terminus and up to 40 amino acids at the C-terminus of the sequence set forth in Figure 15, such that the truncation does not render it unable to interact with FHOS.

5           43. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 250 amino acids at the N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in  
10 Figure 1, such that the truncation does not render it unable to interact with mSWAN;  
or

(c) a sequence having a truncation of up to 250 amino acids at the N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mSWAN,  
15 and wherein said second protein is mSWAN comprising:

(d) an amino acid sequence set forth in Figure 41; or

(e) a sequence having a truncation of up to 859 amino acids at the C-terminus of the sequence set forth in Figure 41, such that the truncation does not render it unable to interact with FHOS.

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44. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 250 amino acids at the  
25 N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m2300003P22Rik(248); or

(c) a sequence having a truncation of up to 250 amino acids at the N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in  
30 Figure 1, such that the truncation does not render it unable to interact with m2300003P22Rik(248),

and wherein said second protein is m2300003P22Rik(248) comprising:

(d) an amino acid sequence set forth in Figure 42; or

(e) a sequence having a truncation of up to 60 amino acids at the

N-terminus of the sequence set forth in Figure 42, such that the truncation does not render it unable to interact with FHOS.

45. The isolated protein complex of Claim 1, wherein said first protein  
5 is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;  
(b) a sequence having a truncation of up to 250 amino acids at the  
N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in  
Figure 1, such that the truncation does not render it unable to interact with  
10 mTAKEDA015; or

(c) a sequence having a truncation of up to 250 amino acids at the  
N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in  
Figure 1, such that the truncation does not render it unable to interact with  
mTAKEDA015,

15 and wherein said second protein is mTAKEDA015 comprising:

(d) an amino acid sequence set forth in Figure 43.

46. The isolated protein complex of Claim 1, wherein said first protein  
is FHOS comprising:

20 (a) an amino acid sequence set forth in Figure 1;  
(b) a sequence having a truncation of up to 250 amino acids at the  
N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in  
Figure 1, such that the truncation does not render it unable to interact with PCNT2; or

(c) a sequence having a truncation of up to 250 amino acids at the  
25 N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in  
Figure 1, such that the truncation does not render it unable to interact with PCNT2,

and wherein said second protein is PCNT2 comprising:

(d) an amino acid sequence set forth in Figure 44; or  
(e) a sequence having a truncation of up to 2941 amino acids at the  
30 N-terminus or up to 202 amino acids at the C-terminus of the sequence set forth in  
Figure 19, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 2941 amino acids at the  
N-terminus and up to 202 amino acids at the C-terminus of the sequence set forth in  
Figure 44, such that the truncation does not render it unable to interact with FHOS.

47. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- 5 (b) a sequence having a truncation of up to 250 amino acids at the N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with KPNA4; or
- (c) a sequence having a truncation of up to 250 amino acids at the N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in
- 10 Figure 1, such that the truncation does not render it unable to interact with KPNA4, and wherein said second protein is KPNA4 comprising:
- (d) an amino acid sequence set forth in Figure 102;
- (e) a sequence having a truncation of up to 106 amino acids at the N-terminus or up to 183 amino acids at the C-terminus of the sequence set forth in
- 15 Figure 102, such that the truncation does not render it unable to interact with FHOS; or
- (f) a sequence having a truncation of up to 106 amino acids at the N-terminus and up to 183 amino acids at the C-terminus of the sequence set forth in Figure 102, such that the truncation does not render it unable to interact with FHOS.

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48. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
  - (b) a sequence having a truncation of up to 250 amino acids at the
  - 25 N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MAPKAP1; or
  - (c) a sequence having a truncation of up to 250 amino acids at the N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in
  - 30 Figure 1, such that the truncation does not render it unable to interact with MAPKAP1,
- and wherein said second protein is MAPKAP1 comprising:
- (d) an amino acid sequence set forth in Figure 103;
  - (e) a sequence having a truncation of up to 355 amino acids at the

N-terminus or up to 6 amino acids at the C-terminus of the sequence set forth in Figure 103, such that the truncation does not render it unable to interact with FHOS;  
or

- (f) a sequence having a truncation of up to 355 amino acids at the  
5 N-terminus and up to 6 amino acids at the C-terminus of the sequence set forth in Figure 103, such that the truncation does not render it unable to interact with FHOS.

49. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- 10 (a) an amino acid sequence set forth in Figure 1;  
(b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mTPT1; or  
(c) a sequence having a truncation of up to 500 amino acids at the  
15 N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mTPT1,  
and wherein said second protein is mTPT1 comprising:  
(d) an amino acid sequence set forth in Figure 47; or  
(e) a sequence having a truncation of up to 15 amino acids at the  
20 C-terminus of the sequence set forth in Figure 47, such that the truncation does not render it unable to interact with FHOS.

50. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- 25 (a) an amino acid sequence set forth in Figure 1;  
(b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mAK014397(679); or  
30 (c) a sequence having a truncation of up to 500 amino acids at the N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mAK014397(679),  
and wherein said second protein is mAK014397(679) comprising:

- (d) an amino acid sequence set forth in Figure 48; or
- (e) a sequence having a truncation of up to 440 amino acids at the N-terminus or up to 39 amino acids at the C-terminus of the sequence set forth in Figure 23, such that the truncation does not render it unable to interact with FHOS; or
- 5 (f) a sequence having a truncation of up to 440 amino acids at the N-terminus and up to 39 amino acids at the C-terminus of the sequence set forth in Figure 48, such that the truncation does not render it unable to interact with FHOS.

51. The isolated protein complex of Claim 1, wherein said first protein  
10 is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with
- 15 mHRMT1L1; or
- (c) a sequence having a truncation of up to 500 amino acids at the N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mHRMT1L1,

20 and wherein said second protein is mHRMT1L1 comprising:

- (d) an amino acid sequence set forth in Figure 49; or
- (e) a sequence having a truncation of up to 18 amino acids at the N-terminus or up to 243 amino acids at the C-terminus of the sequence set forth in Figure 24, such that the truncation does not render it unable to interact with FHOS; or
- 25 (f) a sequence having a truncation of up to 18 amino acids at the N-terminus and up to 243 amino acids at the C-terminus of the sequence set forth in Figure 49, such that the truncation does not render it unable to interact with FHOS.

52. The isolated protein complex of Claim 1, wherein said first protein  
30 is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with



HRMT1L1(241); or

(c) a sequence having a truncation of up to 500 amino acids at the N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with

5 HRMT1L1(241),

and wherein said second protein is HRMT1L1(241) comprising:

(d) an amino acid sequence set forth in Figure 49; or

(e) a sequence having a truncation of up to 1 amino acids at the N-terminus of the sequence set forth in Figure 49, such that the truncation does not  
10 render it unable to interact with FHOS.

53. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

15 (b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with SAT(204);  
or

(c) a sequence having a truncation of up to 500 amino acids at the  
20 N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with SAT(204),  
and wherein said second protein is SAT(204) comprising:

(d) an amino acid sequence set forth in Figure 51; or

(e) a sequence having a truncation of up to 18 amino acids at the  
25 C-terminus of the sequence set forth in Figure 51, such that the truncation does not render it unable to interact with FHOS.

54. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

30 (a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with  
BC023995(305); or

(c) a sequence having a truncation of up to 500 amino acids at the N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with BC023995(305),

5 and wherein said second protein is BC023995(305) comprising:

(d) an amino acid sequence set forth in Figure 52;

(e) a sequence having a truncation of up to 71 amino acids at the N-terminus or up to 11 amino acids at the C-terminus of the sequence set forth in Figure 27, such that the truncation does not render it unable to interact with FHOS; or

10 (f) a sequence having a truncation of up to 71 amino acids at the N-terminus and up to 11 amino acids at the C-terminus of the sequence set forth in Figure 52, such that the truncation does not render it unable to interact with FHOS.

55. The isolated protein complex of Claim 1, wherein said first protein  
15 is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 500 amino acids at the N-terminus or up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with TTN; or

20 (c) a sequence having a truncation of up to 500 amino acids at the N-terminus and up to 414 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with TTN,

and wherein said second protein is TTN comprising:

(d) an amino acid sequence set forth in Figure 53;

25 (e) a sequence having a truncation of up to 26342 amino acids at the N-terminus or up to 615 amino acids at the C-terminus of the sequence set forth in Figure 28, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 26342 amino acids at the N-terminus and up to 615 amino acids at the C-terminus of the sequence set forth in  
30 Figure 53, such that the truncation does not render it unable to interact with FHOS.

56. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 809 amino acids at the N-terminus or up to 64 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mLRRFIP1; or

5 (c) a sequence having a truncation of up to 809 amino acids at the N-terminus and up to 64 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mLRRFIP1,

and wherein said second protein is mLRRFIP1 comprising:

10 (d) an amino acid sequence set forth in Figure 58;

(e) a sequence having a truncation of up to 128 amino acids at the N-terminus or up to 300 amino acids at the C-terminus of the sequence set forth in Figure 58, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 128 amino acids at the  
15 N-terminus and up to 300 amino acids at the C-terminus of the sequence set forth in Figure 58, such that the truncation does not render it unable to interact with FHOS.

57. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

20 (a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 809 amino acids at the N-terminus or up to 64 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mAPC2; or

(c) a sequence having a truncation of up to 809 amino acids at the  
25 N-terminus and up to 64 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mAPC2,

and wherein said second protein is mAPC2 comprising:

(d) an amino acid sequence set forth in Figure 59;

(e) a sequence having a truncation of up to 11 amino acids at the  
30 N-terminus or up to 2126 amino acids at the C-terminus of the sequence set forth in Figure 3, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 11 amino acids at the N-terminus and up to 2126 amino acids at the C-terminus of the sequence set forth in Figure 59, such that the truncation does not render it unable to interact with FHOS.

58. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- 5 (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mCYLN2(1047); or
- 10 (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mCYLN2(1047),

and wherein said second protein is mCYLN2(1047) comprising:

- (d) an amino acid sequence set forth in Figure 60;
- 15 (e) a sequence having a truncation of up to 630 amino acids at the N-terminus or up to 51 amino acids at the C-terminus of the sequence set forth in Figure 60, such that the truncation does not render it unable to interact with FHOS; or
- (f) a sequence having a truncation of up to 630 amino acids at the N-terminus and up to 51 amino acids at the C-terminus of the sequence set forth in
- 20 Figure 60, such that the truncation does not render it unable to interact with FHOS.

59. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
  - 25 (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mACTN3;
- or

- (c) a sequence having a truncation of up to 839 amino acids at the
- 30 N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mACTN3,

and wherein said second protein is mACTN3 comprising:

- (d) an amino acid sequence set forth in Figure 61;
- (e) a sequence having a truncation of up to 354 amino acids at the

N-terminus or up to 392 amino acids at the C-terminus of the sequence set forth in Figure 61, such that the truncation does not render it unable to interact with FHOS; or

- (f) a sequence having a truncation of up to 354 amino acids at the N-terminus and up to 392 amino acids at the C-terminus of the sequence set forth in Figure 61, such that the truncation does not render it unable to interact with FHOS.

60. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mDTNBP1; or
- (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mDTNBP1,

and wherein said second protein is mDTNBP1 comprising:

- (d) an amino acid sequence set forth in Figure 62; or
- (e) a sequence having a truncation of up to 110 amino acids at the C-terminus of the sequence set forth in Figure 62, such that the truncation does not render it unable to interact with FHOS.

61. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mTAKEDA013; or
- (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mTAKEDA013,

and wherein said second protein is mTAKEDA013 comprising:

- (d) an amino acid sequence set forth in Figure 63.

5        62.        The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m14-3-3g;

10        or

- (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m14-3-3g,

and wherein said second protein is m14-3-3g comprising:

- 15        (d) an amino acid sequence set forth in Figure 64; or
- (e) a sequence having a truncation of up to 72 amino acids at the N-terminus of the sequence set forth in Figure 64, such that the truncation does not render it unable to interact with FHOS.

20        63.        The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in

25        Figure 1, such that the truncation does not render it unable to interact with m14-3-3zeta; or

- (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with

30        m14-3-3zeta,

and wherein said second protein is m14-3-3zeta comprising:

- (d) an amino acid sequence set forth in Figure 65; or
- (e) a sequence having a truncation of up to 55 amino acids at the N-terminus of the sequence set forth in Figure 65, such that the truncation does not

render it unable to interact with FHOS.

64. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- 5 (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3zeta;
- or
- 10 (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3zeta, and wherein said second protein is 14-3-3zeta comprising:
- (d) an amino acid sequence set forth in Figure 66;
- 15 (e) a sequence having a truncation of up to 19 amino acids at the N-terminus or up to 35 amino acids at the C-terminus of the sequence set forth in Figure 66, such that the truncation does not render it unable to interact with FHOS; or
- (f) a sequence having a truncation of up to 19 amino acids at the N-terminus and up to 35 amino acids at the C-terminus of the sequence set forth in
- 20 Figure 66, such that the truncation does not render it unable to interact with FHOS.

65. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- 25 (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m14-3-3b;
- or
- (c) a sequence having a truncation of up to 839 amino acids at the
- 30 N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m14-3-3b, and wherein said second protein is m14-3-3b comprising:
- (d) an amino acid sequence set forth in Figure 67;
- (e) a sequence having a truncation of up to 58 amino acids at the

N-terminus or up to 16 amino acids at the C-terminus of the sequence set forth in Figure 67, such that the truncation does not render it unable to interact with FHOS; or

- (f) a sequence having a truncation of up to 58 amino acids at the N-terminus and up to 16 amino acids at the C-terminus of the sequence set forth in Figure 67, such that the truncation does not render it unable to interact with FHOS.

66. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m14-3-3theta; or
- (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with m14-3-3theta,

and wherein said second protein is m14-3-3theta comprising:

- (d) an amino acid sequence set forth in Figure 68; or
- (e) a sequence having a truncation of up to 81 amino acids at the N-terminus of the sequence set forth in Figure 68, such that the truncation does not render it unable to interact with FHOS.

67. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1;
- (b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3theta; or
- (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with 14-3-3theta,



and wherein said second protein is 14-3-3theta comprising:

(d) an amino acid sequence set forth in Figure 69; or

(e) a sequence having a truncation of up to 80 amino acids at the N-terminus of the sequence set forth in Figure 69, such that the truncation does not render it unable to interact with FHOS.

68. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mSPNB2; or

(c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mSPNB2,

and wherein said second protein is mSPNB2 comprising:

(d) an amino acid sequence set forth in Figure 70;

(e) a sequence having a truncation of up to 824 amino acids at the N-terminus or up to 1122 amino acids at the C-terminus of the sequence set forth in Figure 14, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 824 amino acids at the N-terminus and up to 1122 amino acids at the C-terminus of the sequence set forth in Figure 70, such that the truncation does not render it unable to interact with FHOS.

69. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with BC020494(124); or

(c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in

Figure 1, such that the truncation does not render it unable to interact with BC020494(124),

and wherein said second protein is BC020494(124) comprising:

(d) an amino acid sequence set forth in Figure 71.

5

70. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MACF1; or

(c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MACF1,

15 and wherein said second protein is MACF1 comprising:

(d) an amino acid sequence set forth in Figure 72;

(e) a sequence having a truncation of up to 3983 amino acids at the N-terminus or up to 1190 amino acids at the C-terminus of the sequence set forth in Figure 72, such that the truncation does not render it unable to interact with FHOS; or

20 (f) a sequence having a truncation of up to 3983 amino acids at the N-terminus and up to 1190 amino acids at the C-terminus of the sequence set forth in Figure 72, such that the truncation does not render it unable to interact with FHOS.

71. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

25 (a) an amino acid sequence set forth in Figure 1;

(b) a sequence having a truncation of up to 839 amino acids at the N-terminus or up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MYH1; or

30 (c) a sequence having a truncation of up to 839 amino acids at the N-terminus and up to 210 amino acids at the C-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with MYH1,

and wherein said second protein is MYH1 comprising:

(d) an amino acid sequence set forth in Figure 73;

(e) a sequence having a truncation of up to 1559 amino acids at the N-terminus or up to 239 amino acids at the C-terminus of the sequence set forth in Figure 73, such that the truncation does not render it unable to interact with FHOS; or

(f) a sequence having a truncation of up to 1559 amino acids at the N-terminus and up to 239 amino acids at the C-terminus of the sequence set forth in Figure 73, such that the truncation does not render it unable to interact with FHOS.

72. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 950 amino acids at the N-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mPPGB,

and wherein said second protein is mPPGB comprising:

(c) an amino acid sequence set forth in Figure 74;

(d) a sequence having a truncation of up to 31 amino acids at the N-terminus or up to 267 amino acids at the C-terminus of the sequence set forth in Figure 74, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 31 amino acids at the N-terminus and up to 267 amino acids at the C-terminus of the sequence set forth in Figure 74, such that the truncation does not render it unable to interact with FHOS.

73. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

(a) an amino acid sequence set forth in Figure 1; or

(b) a sequence having a truncation of up to 950 amino acids at the N-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mZYX,

and wherein said second protein is mZYX comprising:

(c) an amino acid sequence set forth in Figure 19;

(d) a sequence having a truncation of up to 229 amino acids at the N-terminus or up to 58 amino acids at the C-terminus of the sequence set forth in Figure 75, such that the truncation does not render it unable to interact with FHOS; or

(e) a sequence having a truncation of up to 229 amino acids at the

N-terminus and up to 58 amino acids at the C-terminus of the sequence set forth in Figure 75, such that the truncation does not render it unable to interact with FHOS.

74. The isolated protein complex of Claim 1, wherein said first protein  
5 is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1000 amino acids at the N-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mPRKCABP,

10 and wherein said second protein is mPRKCABP comprising:

- (c) an amino acid sequence set forth in Figure 76; or
- (d) a sequence having a truncation of up to 34 amino acids at the C-terminus of the sequence set forth in Figure 76, such that the truncation does not render it unable to interact with FHOS.

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75. The isolated protein complex of Claim 1, wherein said first protein is FHOS comprising:

- (a) an amino acid sequence set forth in Figure 1; or
- (b) a sequence having a truncation of up to 1000 amino acids at the  
20 N-terminus of the sequence set forth in Figure 1, such that the truncation does not render it unable to interact with mMYLK,

and wherein said second protein is mMYLK comprising:

- (c) an amino acid sequence set forth in Figure 77;
- (d) a sequence having a truncation of up to 567 amino acids at the  
25 N-terminus or up to 664 amino acids at the C-terminus of the sequence set forth in Figure 77, such that the truncation does not render it unable to interact with FHOS; or
- (e) a sequence having a truncation of up to 567 amino acids at the N-terminus and up to 664 amino acids at the C-terminus of the sequence set forth in Figure 77, such that the truncation does not render it unable to interact with FHOS.

30

76. The isolated protein complex of Claim 1, wherein said first protein consists of an amino acid sequence set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117, said second protein consists of an amino acid sequence selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138

77. The isolated protein complex of Claim 1, wherein said first protein is a hybrid protein containing the complete amino acid sequence of FHOS.

5 78. The isolated protein complex of Claim 1, wherein said second protein is a hybrid protein containing the complete amino acid sequence of a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668),  
10 RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241),  
15 SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYG, mPRKCABP and mMYLK.

20 79. The isolated protein complex of Claim 1, wherein said first protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, and 117

80. The isolated protein complex of Claim 1, wherein said second protein comprises an amino acid sequence selected from the group consisting of SEQ  
25 ID NOS: 4-26, 55- 86, and 118-138.

81. A method for making the protein complex of any one of Claims 1-80, comprising the step of providing said first protein and said second protein under conditions such that said first and second proteins contact each other.

30

82. An antibody specific to the protein complex of any one of Claims 1-80.

83. The antibody of Claim 82, wherein said antibody is an scFv

antibody fragment.

84. An isolated protein having a first polypeptide covalently linked to a second polypeptide, the first polypeptide comprising an amino acid sequence set forth  
5 in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117  
or a variant thereof, the second polypeptide comprising an amino acid sequence selected from the group consisting of any of SEQ ID NOS: 4-26, 55- 86, and 118-138;  
or a variant thereof,

wherein the first polypeptide or the variant thereof is capable of interacting  
10 with the second polypeptide or the variant thereof.

85. The isolated protein of claim 84, wherein the variant of the first polypeptide comprises an amino acid sequence selected from the group consisting of:

(a) a first sequence consisting of the amino acids identical to that set  
15 forth in SSEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 the first sequence has one or more conservative amino acid substitutions; and

(b) a second sequence consisting of the amino acids identical to that set  
20 forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 the second sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not alter its interacting property with the second polypeptide.

25

86. The isolated protein of claim 84, wherein the variant of the second polypeptide comprises an amino acid sequence selected from the group consisting of:

(a) a first sequence consisting of the amino acids identical to that set  
30 forth in any of SEQ ID NOS: 4-26, 55- 86, and 118-138; except that, over the entire length corresponding to the amino acid sequence of SEQ ID NOS: 4-26, 55- 86, and 118-138, the first sequence has one or more conservative amino acid substitutions;  
and

(b) a second sequence consisting of the amino acids identical to that set  
forth in any of SEQ ID NOS: 4-26, 55- 86, and 118-138, except that, over the entire

length corresponding to the amino acid sequence of SEQ ID NOS: 4-26, 55- 86, and 118-138, the second sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not alter its interacting property with the first polypeptide.

5

87. The isolated protein of Claim 84, wherein said first polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, and 117, and said second polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138.

10

88. An isolated protein having a first polypeptide and a second polypeptide, the first polypeptide that is FHOS or a variant thereof covalently linked to the second polypeptide selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a variant thereof,

20

25

wherein the first polypeptide or the variant thereof is capable of interacting with the second polypeptide or the variant thereof.

30

89. An isolated protein having a first polypeptide and a second polypeptide, the first polypeptide comprising an amino acid sequence as set forth in Figure 1 or a variant thereof covalently linked to the second polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138 or a variant thereof,

wherein the first polypeptide or the variant thereof is capable of interacting with the second polypeptide or the variant thereof.

90. An isolated protein having a first polypeptide and a second  
5 polypeptide, the first polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 or a variant thereof covalently linked to the second polypeptide comprising an amino acid sequence of a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending,  
10 mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a  
20 variant thereof,

wherein the first polypeptide or the variant thereof is capable of interacting with the second polypeptide or the variant thereof.

91. A nucleic acid encoding the protein of any one of Claims 84-90.

25

92. An antibody specific to the isolated protein of any one of Claims 84-90.

93. A bifunctional antibody specific to FHOS and a protein selected  
30 from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip,



TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3,  
5 mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK.

94. A protein microarray comprising a protein complex having a first  
10 protein which is FHOS or a homologue or derivative or fragment thereof interacting with a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633,  
15 KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN,  
20 mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof.

25 95. The protein microarray of Claim 94, wherein said first protein is FHOS and said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7,  
30 KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN,



- between a first protein which is FHOS or a homologue or derivative or fragment thereof and a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending,
- 5 mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1,
- 10 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or a derivative or a fragment thereof, comprising:
- 15 providing the protein complex;  
contacting said protein complex with a test compound; and  
determining binding of the test compound with said protein complex.

98. The method of Claim 97, wherein said test compound is provided in  
20 a phage display library.

99. The method of Claim 97, wherein said test compound is provided in  
a combinatorial library.

25 100. The method of Claim 97, wherein at least one of said first and second proteins are provided in the protein complex as a hybrid protein having a detectable tag fused thereto.

101. The method of Claim 97, wherein said first protein is FHOS and  
30 said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik,

mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294),  
 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN,  
 m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1,  
 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN,  
 5 mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013,  
 m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2,  
 BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK.

102. A method for selecting modulators of a protein complex formed  
 10 from a first protein which is FHOS or a homologue or derivative or fragment thereof,  
 and a second protein selected from the group consisting of mRNF23, mERp59,  
 mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693,  
 m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending,  
 mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633,  
 15 KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik,  
 mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294),  
 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN,  
 m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1,  
 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN,  
 20 mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013,  
 m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2,  
 BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a  
 homologue or derivative or fragment thereof, comprising:  
 contacting said first protein with said second protein in the presence of a test  
 25 compound; and  
 determining the interaction between said first protein and said second  
 protein.

103. The method of claim 102, wherein the test compound is an agonist  
 30 or an antagonist.

104. The method of claim 103, wherein the agonist or the antagonist  
 comprises a peptide, a small molecule or an organic molecule.

105. The method of claim 103, wherein the antagonist binds to a binding site of the first protein or the second protein, thereby preventing the interaction between the first and the second protein.

5 106. The method of claim 103, wherein the agonist binds to a binding site of the first protein or the second protein thereby promoting the interaction between the first and the second protein.

10 107. The method of Claim 102, wherein said test compound is provided in a phage display library.

108. The method of Claim 102, wherein said test compound is provided in a combinatorial library.

15 109. The method of Claim 102, wherein said first protein is a hybrid protein containing FHOS or a fragment thereof, said second protein is a hybrid protein containing a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, 20 mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, 25 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a fragment thereof.

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110. The method of Claim 102, wherein said interaction between said first protein and said second protein is determined in a cell.

111. The method of Claim 110, wherein said cell is a yeast cell.

112. The method of Claim 102, wherein said step of determining the interaction between said first protein and said second protein is conducted in a substantially cell free environment.

5

113. A method for screening to identify compounds that promotes or that inhibits a binding affinity of a protein complex formed between a first protein which is FHOS or a homologue or derivative or fragment thereof and a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK or a homologue or a derivative or a fragment thereof, the method comprising:

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(a) contacting a composition comprising said protein complex with a test compound to be screened under conditions to permit interaction between the compound and said protein complex; and

(b) determining the binding affinity of said protein complex after step (a).

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114. The method of claim 113, wherein the test compound is an agonist or an antagonist.

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115. The method of claim 114, wherein the agonist or the antagonist comprises a peptide, a small molecule or an organic molecule.

116. The method of claim 114, wherein the antagonist binds to a binding

site of the protein complex, thereby inhibiting normal biological activity of the protein complex.

117. The method of claim 114, wherein the agonist binds to a binding site  
5 of the protein complex, thereby promoting normal biological activity of the protein complex.

118. A method for screening to identify compounds that activate or that  
inhibit an activity of a protein complex formed between a first protein which is FHOS  
10 or a homologue or derivative or fragment thereof and a second protein selected from  
the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP,  
mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1,  
mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6,  
KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL,  
15 mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip,  
TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87),  
mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2,  
KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241),  
SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3,  
20 mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b,  
m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB,  
mZYGX, mPRKCABP and mMYLK, or a homologue or a derivative or a fragment  
thereof, the method comprising:

- (a) measuring the activity of said protein complex in the presence of a  
25 candidate compound;
- (b) measuring the activity of said protein complex in the absence of the  
candidate compound; and
- (c) detecting the effect of the candidate compound by comparing the  
activity in (a) and (b).

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119. The method of Claim 118, wherein said candidate compound is  
provided in a phage display library.

120. The method of Claim 118, wherein said candidate compound is

provided in a combinatorial library.

121. The method of Claim 118, wherein at least one of said first and second proteins are provided in the protein complex as a hybrid protein having a detectable tag fused thereto.

122. The method of Claim 118, wherein said first protein is FHOS and said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), , mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK.

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123. A method for determining whether a compound is capable of modulating an interaction between a first polypeptide and a second polypeptide, said first polypeptide being FHOS or a homologue or derivative or fragment thereof and said second polypeptide being selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2,

30



BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP, mMYLK or a homologue or derivative or fragment thereof, said method comprising:

- (a) expressing in an isolated host cell in the presence of a test compound, a first hybrid protein having a DNA binding domain fused to said first polypeptide, a second hybrid protein having a transcription-activating domain fused to said second polypeptide and a reporter gene, wherein the expression of the reporter gene is dependent on the interaction between the first polypeptide and the second polypeptide; and
- (b) detecting the expression of said reporter gene.

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124. A method for determining whether a compound is capable of modulating an interaction between a first polypeptide and a second polypeptide, said first polypeptide being FHOS or a homologue or derivative or fragment thereof and said second polypeptide being selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK, or a homologue or derivative or fragment thereof, said method comprising:

- (a) expressing in an isolated host cell in the presence of a test compound, a first hybrid protein having a transcription-activating domain fused to said first polypeptide, a second hybrid protein having a DNA binding domain fused to said second polypeptide and a reporter gene, wherein the expression of the reporter gene is dependent on the interaction between the first polypeptide and the second polypeptide; and
- (b) detecting the expression of said reporter gene.

30

125. A composition comprising:  
a first expression vector having a nucleic acid encoding FHOS or a  
homologue or derivative or fragment thereof; and  
a second expression vector having a nucleic acid encoding a protein selected  
5 from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP,  
mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1,  
mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6,  
KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL,  
mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip,  
10 TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87),  
mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2,  
KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241),  
SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3,  
mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b,  
15 m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB,  
mZYGX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof.

126. An isolated host cell comprising:  
a first expression vector having a first nucleic acid encoding a first protein  
20 which is FHOS or a homologue or derivative or fragment thereof; and  
a second expression vector having a second nucleic acid encoding a second  
protein selected from the group consisting of mRNF23, mERp59, mBRD7(621),  
mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693,  
m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending,  
25 mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633,  
KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik,  
mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294),  
14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN,  
m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1,  
30 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN,  
mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013,  
m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2,  
BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK, or a  
homologue or derivative or fragment thereof.

127. The isolated host cell of Claim 126, wherein said first protein is FHOS.

5           128. The isolated host cell of Claim 126, wherein said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, 10 mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, 15 mDTNBPI, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK.

          129. The isolated host cell of Claim 126, wherein said first protein is 20 FHOS, and said second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), 25 m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBPI, mTAKEDA013, 30 m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK.

130. The isolated host cell of Claim 126, wherein said first protein comprises an amino acid sequence selected from the group consisting of:

(a) a first sequence consisting of the amino acids as set forth in Figure 1;

(b) a second sequence consisting of the amino acids as set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117;

5 (c) a third sequence consisting of the amino acids identical to that set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117, the third sequence has one or more conservative amino acid substitutions;

10 (d) a fourth sequence consisting of the amino acids identical to that set forth in SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 except that, over the entire length corresponding to the amino acid sequence of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117, the fourth sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence  
15 which do not alter its interacting property with the second protein;

(e) a fifth sequence consisting of the amino acids identical to that set forth in Figure 1 except that, over the entire length corresponding to the amino acid sequence of Figure 1, the fifth sequence has one or more conservative amino acid substitutions; and

20 (f) a sixth sequence consisting of the amino acids identical to that set forth in Figure 1 except that, over the entire length corresponding to the amino acid sequence of Figure 1, the sixth sequence has one or more non-conservative amino acid substitutions, deletions or insertions at such positions of the amino acid sequence which do not alter its interacting property with the second protein.

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131. The isolated host cell of Claim 126, wherein said second protein comprises an amino acid sequence selected from the group consisting of:

(a) a first sequence consisting of the amino acids as set forth in in any of Figures 2 -23, 27-53, and 58-77; (b) a second sequence consisting of the amino  
30 acids as set forth in any of SEQ ID NOS: 4-26, 55- 86, and 118-138;

(c) a third sequence consisting of the amino acids identical to that set forth in any of SEQ ID NOS: 4-26, 55- 86, and 118-138,except that, over the entire length corresponding to the amino acid sequence of SEQ ID NOS: 4-26, 55- 86, and 118-138, the third sequence has one or more conservative amino acid substitutions;

(d) a fourth sequence consisting of the amino acids identical to that set forth in any of SEQ ID NOS: 4-26, 55- 86, and 118-138, except that, over the entire length corresponding to the amino acid sequence of SEQ ID NOS: 4-26, 55- 86, and 118-138, the fourth sequence has one or more non-conservative amino acid  
5 substitutions, deletions or insertions at such positions of the amino acid sequence which do not render it unable to interact with the first protein;

(e) a fifth sequence consisting of the amino acids identical to that set forth in in any of Figures 2 -23, 27-53, and 58-77, except that, over the entire length corresponding to the amino acid sequence of Figures 2 -23, 27-53, and 58-77, the fifth  
10 sequence has one or more conservative amino acid substitutions; and

(f) a sixth sequence consisting of the amino acids identical to that set forth in in any of Figures 2 -23, 27-53, and 58-77, except that, over the entire length corresponding to the amino acid sequence of Figures 2 -23, 27-53, and 58-77, ; the sixth sequence has one or more non-conservative amino acid substitutions, deletions  
15 or insertions at such positions of the amino acid sequence which do not render it unable to interact with the first protein.

132. The isolated host cell of Claim 126, wherein said first protein consists of an amino acid sequence selected from the group consisting of SEQ ID NO:  
20 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117 said second protein consists of an amino acid sequence selected from the group consisting of any of SEQ ID NOS: 4-26, 55- 86, and 118-138;

133. The isolated host cell of Claim 126, wherein said first protein  
25 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 51, 52, 53, 54, 115, 116, or 117.

134. The isolated host cell of Claim 126, wherein said second protein comprises an amino acid sequence selected from the group consisting of any of SEQ  
30 ID NOS: 4-26, 55- 86, and 118-138,

135. The isolated host cell of Claim 126, wherein said cell is a yeast cell.

136. The isolated host cell of Claim 126, wherein said cell is a

mammalian cell.

137. The isolated host cell of Claim 126, wherein one of said first and second nucleic acids is linked to a nucleic acid encoding a DNA binding domain, and the other of said first and second nucleic acids is linked to a nucleic acid encoding a transcription-activation domain, whereby two hybrid proteins can be produced in said cell.

138. The isolated host cell of Claim 137, further comprising a reporter gene, wherein the transcription of the reporter gene is dependent on the interaction between the first polypeptide and the second polypeptide.

139. The isolated host cell of Claim 138, wherein said reporter gene encodes an auxotrophic factor.

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140. The isolated host cell of Claim 138, wherein said reporter gene encodes a protein that inhibits the growth of said isolated host cell under a predetermined condition.

141. The isolated host cell of Claim 138, wherein said reporter gene encodes a cytotoxic toxin.

142. A method for modulating the function or activity of a protein complex in cells of a specific tissue of a mammal, said protein complex having a first protein which is FHOS or a homologue or derivative or fragment thereof interacting with a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN,

mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof, said method comprising:

- 5           delivering to the specific tissue, a selected compound for modulating the function or activity of said protein complex.

143.     The method of Claim 142, wherein said compound is an antibody.

- 10           144.     The method of Claim 143, wherein said antibody is specific to the protein complex.

145.     The method of Claim 142, wherein said compound interferes with the interaction between said first protein and said second protein.

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146.     The method of Claim 142, wherein said compound enhances the interaction between said first protein and said second protein.

147.     A method for screening for compounds that selectively modulate a biological function selected from the group consisting of signal transduction, cytoskeleton rearrangement, membrane trafficking, cell polarity, cell movement, transcription activation or inhibition, protein synthesis and cell-cycle regulation, the method comprising:

- 20           (a)     delivering a compound to be screened to a cell population of a first kind, wherein the first kind of the cell population shows abnormality in said biological function under a set of culture conditions sufficient for other cell population not to show said abnormality wherein said abnormality is due to an aberration in a protein complex or an interaction thereof between FHOS and a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, 25 mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, 30 TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87),

- mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof;
- 5     (b)     delivering the compound to a cell population of a second kind that is not known to show said abnormality under said conditions and not known to have said aberration, wherein the compound does not affect said biological function of the
- 10    second kind of the cell population;
- (c)     comparing said biological function of the first and second kinds of cell populations; and
- (d)     selecting the compound that inhibits said abnormal biological function of the first kind of cell population comparable to that of the second kind of
- 15    cell population.

148.     The method of claim 147 further comprising administering the selected compound after step (d) to a subject in need of said compound wherein the subject is selected from the group consisting of mammals, tissue explants, and

20    individual cells.

149.     A method of screening for potential therapeutic compounds that selectively modulate abnormality in a biological function selected from the group consisting of signal transduction, cytoskeleton rearrangement, membrane trafficking,

25    cell polarity, cell movement, transcription activation or inhibition, protein synthesis and cell-cycle regulation, the method comprising:

- (a)     administering a compound to be screened to a transgenic FHOS-null non-human animal model expressing a mutated human FHOS protein that fails to interact with or interacts aberrantly with a protein selected from the group consisting
- 30    of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144,



ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK, or a homologue or derivative or fragment thereof leading to symptoms associated with a physiological disorder selected from the group consisting of diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers and neurodegenerative disorders; and

(b) selecting the compound that effectuates recovery of the transgenic animal from symptoms associated with said physiological disorder.

150. The method of claim 149, wherein the compound is administered by intra-tissue infusion.

151. A method for screening for potential therapeutic compounds that selectively modulate abnormality in a biological function selected from the group consisting of signal transduction, cytoskeleton rearrangement, membrane trafficking, cell polarity, cell movement, transcription activation or inhibition, protein synthesis or cell-cycle regulation, the method comprising:

(a) administering a compound to be screened to a first transgenic FHOS-null non-human animal model expressing a mutated human FHOS protein that fails to interact with or interacts aberrantly with a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3,

- mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK, or a homologue or derivative or fragment thereof leading to symptoms associated with a physiological disorder selected from the group consisting of diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers and neurodegenerative disorders;
- (b) administering the compound to a second transgenic FHOS-null non-human animal model expressing a wild-type human FHOS protein that interacts with the protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof, wherein said compound does not affect said biological function in the second transgenic animal model; and
- (c) selecting the compound that effectuates recovery of the first transgenic animal from symptoms associated with said physiological disorder as revealed by the comparisons between the first and second transgenic animals.

152. A method for modulating a biological function selected from the group consisting of signal transduction, cytoskeleton rearrangement, membrane trafficking, cell polarity, cell movement, transcription activation or inhibition, protein synthesis and cell-cycle regulation in a patient, comprising:

administering to the patient a selected compound for modulating the function or activity of a protein complex having a first protein which is FHOS or a homologue or derivative or fragment thereof interacting with a second protein selected from the

group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof.

153. The method of Claim 152, wherein said compound is an antibody.

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154. The method of Claim 153, wherein said antibody is specific to the protein complex.

155. The method of Claim 152, wherein said compound interferes with the interaction between said first protein and said second protein.

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156. The method of Claim 152, wherein said compound enhances the interaction between said first protein and said second protein.

157. A method for modulating a biological function selected from the group consisting of signal transduction, cytoskeleton rearrangement, membrane trafficking, cell polarity, cell movement, transcription activation or inhibition, protein synthesis and cell-cycle regulation in a patient, comprising:

25

modulating the function or activity of a protein complex having a first protein which is FHOS or a homologue or derivative or fragment thereof interacting with a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633,

30

KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, 5 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof.

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158. The method of Claim 157, wherein said modulating step comprises increasing the protein complex level.

159. The method of Claim 158, wherein the level of the protein complex 15 is increased by administering to the patient a therapeutically effective amount of said protein complex.

160. The method of Claim 158, wherein said increasing step comprises administering to the patient one of the first protein and the second protein or both.

20

161. The method of Claim 159, wherein said increasing step comprises administering to the patient a nucleic acid encoding said first protein, or a nucleic acid encoding said second protein, or both.

25 162. The method of Claim 159, wherein said increasing step comprises administering to the patient a plurality of cells expressing said protein complex.

163. The method of Claim 157, wherein said modulating step comprises reducing the protein complex level.

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164. The method of Claim 158, wherein said reducing step comprises administering to the patient an antibody against said first protein or an antibody against said second protein, or both, or an antibody specific to the protein complex.

165. The method of Claim 158, wherein said reducing step comprises administering to the patient an antisense compound capable of interfering with the expression of said first or second protein or both.

5 166. The method of Claim 158, wherein said reducing step comprises administering to the patient a ribozyme specific against an mRNA encoding said first protein or an mRNA encoding said second protein, or both.

10 167. The method of Claim 158, wherein said reducing step comprises administering to the patient a peptide nucleic acid (PNA) capable of specifically binding to an mRNA encoding said first protein or an mRNA encoding said second protein, or both.

15 168. The method of Claims 152-167, which is used to treat a physiological disorder associated with diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers or neurodegenerative disorders.

20 169. A method for the treatment of a patient having a need to inhibit the interaction of FHOS or a homologue or derivative or fragment thereof with a protein required to form a protein complex in the cells associated with diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers or neurodegenerative disorders of the patient, the method comprising administering to  
25 the patient a therapeutically effective amount of an agonist or an antagonist targeted to the cells associated with diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers or neurodegenerative disorders, wherein the agonist or the antagonist binds to FHOS or a homologue or derivative or fragment thereof, the  
30 second protein or the protein complex and inhibits the interaction, wherein the second protein is selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633,

KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, 5 mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or a homologue or derivative or fragment thereof.

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170. The method of claim 169, wherein the agonist or the antagonist binds to a binding site of the first protein or the second protein, thereby preventing the interaction between the first and the second protein.

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171. The method of claim 169, wherein the agonist or the antagonist comprises a peptide or an organic molecule.

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172. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a protein complex having a human FHOS interacting with a human protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), 25 m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, 30 m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK.

173. A pharmaceutical composition comprising FHOS and a protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1,

mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, 5 TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, 10 m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK in a combined amount that is therapeutically or prophylactically effective, and a pharmaceutically acceptable carrier.

174. A pharmaceutical composition comprising an antibody specific to 15 FHOS and an antibody specific to a protein selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138, in a combined amount that is therapeutically or prophylactically effective, and a pharmaceutically acceptable carrier.

175. A method of isolating, from a sample, FHOS comprising: 20 contacting said sample with a second protein comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 4-26, 55- 86, and 118-138; and isolating a protein complex comprising FHOS and said second protein.

25 176. A method of detecting, in a sample, FHOS comprising: contacting said sample with a second protein comprising an amino acid sequence selected from the group consisting of any of SEQ ID NOS: 4-26, 55- 86, and 118-138; and detecting a protein complex comprising FHOS and said second protein.

30 177. A method of isolating, from a sample, a first protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6,

KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 and 37, SEQ ID NO: 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 and 25 comprising:

5           contacting said sample with a second protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2 and 3; 1,2,3,4,5, SEQ ID NO: 1, 2, 3 and 4 and

          isolating a protein complex comprising said first protein and said second protein.

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178.     A method of detecting, in a sample, a first protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305) and TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK comprising:

25           contacting said sample with a second protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1, 2 and 3, 1, 2, 3, 4 and 5;; SEQ ID NO: 1, 2, 3 and 4 and

          detecting a protein complex comprising the first protein and said second protein.

30           179.     A method for diagnosing a physiological disorder associated with diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers or neurodegenerative disorders or a predisposition to the disorder in a patient, comprising:



detecting, in said patient, any aberration of a protein complex having a first protein which is FHOS interacting with a second protein selected from the group consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1,  
5 mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, of mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2,  
10 KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYGX, mPRKCABP and mMYLK

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180. The method of Claim 179, wherein said detecting step comprises detecting an aberrant level of said protein complex in a tissue sample from said patient.

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181 The method of Claim 179, wherein said detecting step comprises detecting an aberrant binding affinity between said first protein and said second protein.

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182. The method of Claim 179, wherein said detecting step comprises determining the level of said first protein or said second protein or both in a tissue sample from said patient.

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183. The method of Claim 179, wherein said detecting step comprises determining the level of the mRNAs encoding said first protein or said second protein or both in a tissue sample from said patient.

184. The method of Claim 179, wherein said detecting step comprises detecting an aberrant localization of said protein complex in a cell from said patient.

185. The method of Claim 179, wherein said detecting step comprises detecting a mutation in a gene encoding said first or second protein.

186. A kit for use in diagnosing a physiological disorder associated with  
5 diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers or neurodegenerative disorders in a patient, comprising, in a compartmentalized carrier, an antibody specific to a protein complex having a first protein which is FHOS interacting with a second protein selected from the group  
10 consisting of mRNF23, mERp59, mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, of mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip,  
15 TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b,  
20 m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK

187. A kit for use in diagnosing a physiological disorder associated with diabetes mellitus, cardiovascular disease, hypertension, nephropathy, acute and  
25 chronic inflammatory disorders, autoimmune diseases, cell proliferative disorders, cancers or neurodegenerative disorders in a patient, comprising, in a compartmentalized carrier, a first oligonucleotide selectively hybridizable to the mRNA encoding FHOS and a second oligonucleotide selectively hybridizable to the mRNA encoding a protein selected from the group consisting of mRNF23, mERp59,  
30 mBRD7(621), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, of mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144,

ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013,  
 5 m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK.

188. An isolated polypeptide selected from the group consisting of:
- (a) a first polypeptide comprising the amino acid sequence set forth in  
 10 SEQ ID NO: 6, 10, 25, 30, 46, 57, 65, 75, 82, 88, 107; 120, 123, 132 or 141
  - (b) a second polypeptide which is the amino acid sequence set forth in  
 SEQ ID NO: 6, 10, 25, 30 or 46, 57, 65, 75, 82, 88 or 107; 120, 123, 132 or 141;
  - (c) a third polypeptide which is encoded by a polynucleotide  
 comprising a polynucleotide sequence of SEQ ID NO: 48, 49, 50, 111, 112, 113, 114;  
 15 157, 158 or 159;
  - (d) a fourth polypeptide consisting of the amino acids identical to that  
 set forth in SEQ ID NO: 6, 10, 25, 30, 46, 57, 65, 75, 82, 88, 107; 120, 123, 132 or  
 141 except that, over the entire length corresponding to the amino acid sequence in  
 SEQ ID NO: 6, 10, 25, 30, 46, 57, 65, 75, 82, 88, 107; 120, 123, 132 or 141; the  
 20 fourth sequence has one or more conservative amino acid substitutions; and
  - (e) a fifth polypeptide consisting of the amino acids identical to that set  
 forth in SEQ ID NO: 6, 10, 25, 30, 46, 57, 65, 75, 82, 88, 107; 120, 123, 132 or 141  
 except that, over the entire length corresponding to the amino acid sequence in SEQ  
 ID NO: 6, 10, 25, 30, 46, 57, 65, 75, 82, 88, 107; 120, 123, 132 or 141 the fifth  
 25 sequence has one or more non-conservative amino acid substitutions, deletions or  
 insertions at such positions of the amino acid sequence which do not alter its  
 interacting property with a protein which is FHOS or a homologue or derivative or  
 fragment thereof.

- 30 189. An isolated polynucleotide segment, comprising a polynucleotide  
 sequence selected from the group consisting of:
- (a) a first sequence having nucleotides 1 to 807 of SEQ ID NO: 48; 1 to  
 348 of SEQ ID NO: 49 or 1 to 1281 of SEQ ID NO: 50;
  - (b) a second sequence consisting of the nucleotides identical to that set

forth in SEQ ID NO: 48, 49 or 50 except that, over the entire length corresponding to the nucleotide sequence of SEQ ID NO: 48, 49 or 50, the second sequence has one or more nucleotide substitutions, deletions or insertions;

5 (c) a third sequence obtained by screening an appropriate library under stringent hybridization conditions with a probe which is a segment of 15 or more nucleotides of SEQ ID NO: 48, 49 or 50 wherein the third sequence encodes a polypeptide identical to mBRD7(621), mTAKEDA009 or KIAA1288(1191) or a variant thereof;

10 (d) a fourth sequence that encodes a polypeptide sequence set forth in SEQ ID NO: 6, 10, 25, 30 or 46; and

(e) a fifth sequence that encodes a truncated polypeptide of the polypeptide sequence set forth in SEQ ID NO: 6, 10, 25, 30 or 46 wherein the polypeptide or the truncated polypeptide encoded by the polynucleotide sequence interacts with FHOS.

15 190. An isolated polynucleotide segment, comprising a polynucleotide sequence selected from the group consisting of:

(a) a first sequence having nucleotides 1 to 486 of SEQ ID NO: 111; 1 to 891 of SEQ ID NO: 112; 1 to 783 of SEQ ID NO: 113 or 1 to 723 of SEQ ID NO: 20 114;

(b) a second sequence consisting of the nucleotides identical to that set forth in SEQ ID NO: 111, 112, 113 or 114 except that, over the entire length corresponding to the nucleotide sequence of SEQ ID NO: 111, 112, 113 or 114, the second sequence has one or more nucleotide substitutions, deletions or insertions;

25 (c) a third sequence obtained by screening an appropriate library under stringent hybridization conditions with a probe which is a segment of 15 or more nucleotides of SEQ ID NO: 111, 112, 113 or 114 wherein the third sequence encodes a polypeptide identical to mBC026864(777), ZNF144(294), mTAKEDA015 or HRMT1L1(241) or a variant thereof;

30 (d) a fourth sequence that encodes a polypeptide sequence set forth in SEQ ID NO: 57, 65, 75, 82, 88 or 107; and

(e) a fifth sequence that encodes a truncated polypeptide of the polypeptide sequence set forth in SEQ ID NO: 57, 65, 75, 82, 88 or 107 wherein the polypeptide or the truncated polypeptide encoded by the

polynucleotide sequence interacts with FHOS.

191. An isolated polynucleotide segment, comprising a polynucleotide sequence selected from the group consisting of:

5 (a) a first sequence having nucleotides 1 to 1098 of SEQ ID NO: 157; 1 to 591 of SEQ ID NO: 158 or 1 to 375 of SEQ ID NO: 159.

(b) a second sequence consisting of the nucleotides identical to that set forth in SEQ ID NO: 157, 158 or 159 except that, over the entire length corresponding to the nucleotide sequence of SEQ ID NO: 157, 158 or 159, the second sequence has  
10 one or more nucleotide substitutions, deletions or insertions;

(c) a third sequence obtained by screening an appropriate library under stringent hybridization conditions with a probe which is a segment of 15 or more nucleotides of SEQ ID NO: 157, 158 or 159 wherein the third sequence encodes a polypeptide identical to mCYLN2(1047), mTAKEDA013 and BC020494(124) or a  
15 variant thereof;

(d) a fourth sequence that encodes a polypeptide sequence set forth in SEQ ID NO: 120, 123, 132 or 141; and

(e) a fifth sequence that encodes a truncated polypeptide of the polypeptide sequence set forth in SEQ ID NO: 120, 123, 132 or 141;

20 wherein the polypeptide or the truncated polypeptide encoded by the polynucleotide sequence interacts with FHOS.